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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=2; day=19; hr=9; min=42; sec=47; ms=323;]

=====

Reviewer Comments:

1.

E355 Empty lines found between the amino acid numbering and the proteins SEQID (11)

E321 No. of Bases conflict, this line has no nucleotides SEQID (11) POS (126)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (12)

E321 No. of Bases conflict, this line has no nucleotides SEQID (12) POS (0)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (12)

E321 No. of Bases conflict, this line has no nucleotides SEQID (12) POS (512)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (22)

E321 No. of Bases conflict, this line has no nucleotides SEQID (22) POS (112)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (24)

E321 No. of Bases conflict, this line has no nucleotides SEQID (24) POS (496)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (28)

E321 No. of Bases conflict, this line has no nucleotides SEQID (28) POS (16)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (30)

E321 No. of Bases conflict, this line has no nucleotides SEQID (30) POS (48)

<210> 11
 <211> 1582
 <212> DNA
 <213> Zea mays
 <220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form
 <220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.
 <220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.
 <220>
 <221> variation
 <222> (1578)
 <223> k = g or t.
 * * * * *

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	

For SEQ ID # 11, 12, 22, 24, 28, and 30 the sequence rules specify the numbering for amino acids be placed below the line of amino acids in a protein or coding region of a nucleotide sequence.

"Sec. 1.822 Symbols and format to be used for nucleotide and/or amino acid sequence data.

(a) The symbols and format to be used for nucleotide and/or amino

acid sequence data shall conform to the requirements of paragraphs (b) through (e) of this section.

(d) Representation of amino acids. (1) The amino acids in a protein or peptide sequence shall be listed using the three-letter abbreviation with the first letter as an upper case character, as in WIPO Standard ST.25 (1998), Appendix 2, Table 3.

(4) The enumeration of amino acids may start at the first amino acid of the first mature protein, with the number 1. When presented, the amino acids preceding the mature protein, e.g., pre-sequences, pro-sequences, pre-pro-sequences and signal sequences, shall have negative numbers, counting backwards starting with the amino acid next to number 1. Otherwise, the enumeration of amino acids shall start at the first amino acid at the amino terminal as number 1. It shall be marked below the sequence every 5 amino acids."

In the SEQ ID numbers listed above there are blank lines found between the amino acids and the numbering for the amino acids at different locations. Please remove all blank lines found between the amino acids and the numbering in these sequences.

2.

E300	Invalid codon found Asn SEQID (11) POS: 388
E300	Invalid codon found Ser SEQID (11) POS: 391
E300	Invalid codon found Gly SEQID (11) POS: 394
E300	Invalid codon found Ile SEQID (11) POS: 397
E300	Invalid codon found Asn SEQID (11) POS: 400
E300	Invalid codon found Lys SEQID (11) POS: 403
E300	Invalid codon found Ile SEQID (11) POS: 406
E300	Invalid codon found Phe SEQID (11) POS: 409
E300	Invalid codon found Val SEQID (11) POS: 412
E300	Invalid codon found Met SEQID (11) POS: 415
E300	Invalid codon found Ser SEQID (11) POS: 418
E300	Invalid codon found Gln SEQID (11) POS: 421
E300	Invalid codon found Phe SEQID (11) POS: 424
E300	Invalid codon found Asn SEQID (11) POS: 427
E300	Invalid codon found Ser SEQID (11) POS: 430
E300	Invalid codon found Thr SEQID (11) POS: 433

The errors shown above are ok and require no response.

Application No: 10569000 Version No: 1.0

Input Set:**Output Set:**

Started: 2010-02-18 13:09:42.494
Finished: 2010-02-18 13:09:51.451
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms
Total Warnings: 0
Total Errors: 302
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 300	Invalid codon found Asn SEQID (11) POS: 388
E 300	Invalid codon found Ser SEQID (11) POS: 391
E 300	Invalid codon found Gly SEQID (11) POS: 394
E 300	Invalid codon found Ile SEQID (11) POS: 397
E 300	Invalid codon found Asn SEQID (11) POS: 400
E 300	Invalid codon found Lys SEQID (11) POS: 403
E 300	Invalid codon found Ile SEQID (11) POS: 406
E 300	Invalid codon found Phe SEQID (11) POS: 409
E 300	Invalid codon found Val SEQID (11) POS: 412
E 300	Invalid codon found Met SEQID (11) POS: 415
E 300	Invalid codon found Ser SEQID (11) POS: 418
E 300	Invalid codon found Gln SEQID (11) POS: 421
E 300	Invalid codon found Phe SEQID (11) POS: 424
E 300	Invalid codon found Asn SEQID (11) POS: 427
E 300	Invalid codon found Ser SEQID (11) POS: 430
E 300	Invalid codon found Thr SEQID (11) POS: 433
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12)

Input Set :

Output Set :

Started: 2010-02-18 13:09:42.494

Finished: 2010-02-18 13:09:51.451

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms

Total Warnings: 0

Total Errors: 302

No. of SeqIDs Defined: 42

Actual SeqID Count: 42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed

Input Set:

Output Set:

Started: 2010-02-18 13:09:42.494
Finished: 2010-02-18 13:09:51.451
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms
Total Warnings: 0
Total Errors: 302
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
Hannah, L. Curtis
Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<140> 10569000

<141> 2010-02-18

<150> US 60/496,188

<151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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<211> 1425

<212> DNA

<213> zea mays

<400> 1

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gctcatgata gtgttcttgg aatcattctg ggaggtgggtg ctgggactag attgtacccc	180
ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat	240
attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaatth	300
aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac	360
aagaatgaag ggtttggtga agtcttagct gcacagcaga gccagataa tccaaactgg	420
tttcagggta ctgcagatgc tgtaaggcag tacttgtggt tgtttgagga gcataatgtg	480
atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt	540
caggcacaca gagaacaaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa	600
cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct	660
gagaaaccga aaggagagca gttgaaagca atgatgggtg acaccaccat acttggcctt	720
gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc	780
aaagatgtaa tgcttcagct cctccgtgaa caatttctctg aagccaatga ctttggaagt	840
gaggttattc caggtgcaac cagcattgga aagaggggttc aggcttatct gtatgatggt	900
tactgggaag atacgggtac cattgcccga ttttataatg caaacttggg aataaccaag	960

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gaaggtgcta tcatagagga cagtttacta atgggtgagg actactatga gacagaagct 1200
gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc 1260
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gtcacagtga tcaaggatgc ttactccct agtgggaacag ttata 1425

<210> 2
<211> 475
<212> PRT
<213> zea mays

<400> 2

Met	Asp	Met	Ala	Leu	Ala	Ser	Lys	Ala	Ser	Pro	Pro	Pro	Trp	Asn	Ala	1	5	10	15
Thr	Ala	Ala	Glu	Gln	Pro	Ile	Pro	Lys	Arg	Asp	Lys	Ala	Ala	Ala	Asn	20	25	30	
Asp	Ser	Thr	Tyr	Leu	Asn	Pro	Gln	Ala	His	Asp	Ser	Val	Leu	Gly	Ile	35	40	45	
Ile	Leu	Gly	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Lys	Lys	50	55	60	
Arg	Ala	Lys	Pro	Ala	Val	Pro	Leu	Gly	Ala	Asn	Tyr	Arg	Leu	Ile	Asp	65	70	75	80
Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	Ile	Tyr	Val	85	90	95	
Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Leu	Ser	Arg	Ala	100	105	110	
Tyr	Gly	Ser	Asn	Ile	Gly	Gly	Tyr	Lys	Asn	Glu	Gly	Phe	Val	Glu	Val	115	120	125	
Leu	Ala	Ala	Gln	Gln	Ser	Pro	Asp	Asn	Pro	Asn	Trp	Phe	Gln	Gly	Thr	130	135	140	
Ala	Asp	Ala	Val	Arg	Gln	Tyr	Leu	Trp	Leu	Phe	Glu	Glu	His	Asn	Val	145	150	155	160
Met	Glu	Phe	Leu	Ile	Leu	Ala	Gly	Asp	His	Leu	Tyr	Arg	Met	Asp	Tyr	165	170	175	

Glu	Lys	Phe	Ile	Gln	Ala	His	Arg	Glu	Thr	Asn	Ala	Asp	Ile	Thr	Val	180	185	190
Ala	Ala	Leu	Pro	Met	Asp	Glu	Lys	Arg	Ala	Thr	Ala	Phe	Gly	Leu	Met	195	200	205
Lys	Ile	Asp	Glu	Glu	Gly	Arg	Ile	Ile	Glu	Phe	Ala	Glu	Lys	Pro	Lys	210	215	220
Gly	Glu	Gln	Leu	Lys	Ala	Met	Met	Val	Asp	Thr	Thr	Ile	Leu	Gly	Leu	225	230	235
Asp	Asp	Val	Arg	Ala	Lys	Glu	Met	Pro	Tyr	Ile	Ala	Ser	Met	Gly	Ile	245	250	255
Tyr	Val	Phe	Ser	Lys	Asp	Val	Met	Leu	Gln	Leu	Leu	Arg	Glu	Gln	Phe	260	265	270
Pro	Glu	Ala	Asn	Asp	Phe	Gly	Ser	Glu	Val	Ile	Pro	Gly	Ala	Thr	Ser	275	280	285
Ile	Gly	Lys	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Glu	Asp	290	295	300
Ile	Gly	Thr	Ile	Ala	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	Thr	Lys	305	310	315
Lys	Pro	Ile	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Phe	Ala	Pro	Ile	Tyr	325	330	335
Thr	Gln	Pro	Arg	His	Leu	Pro	Pro	Ser	Lys	Val	Leu	Asp	Ala	Asp	Val	340	345	350
Thr	Asp	Ser	Val	Ile	Gly	Glu	Gly	Cys	Val	Ile	Lys	Asn	Cys	Lys	Ile	355	360	365
Asn	His	Ser	Val	Val	Gly	Leu	Arg	Ser	Cys	Ile	Ser	Glu	Gly	Ala	Ile	370	375	380
Ile	Glu	Asp	Ser	Leu	Leu	Met	Gly	Ala	Asp	Tyr	Tyr	Glu	Thr	Glu	Ala	385	390	395
Asp	Lys	Lys	Leu	Leu	Ala	Glu	Lys	Gly	Gly	Ile	Pro	Ile	Gly	Ile	Gly	405	410	415
Lys	Asn	Ser	Cys	Ile	Arg	Arg	Ala	Ile	Ile	Asp	Lys	Asn	Ala	Arg	Ile	420	425	430
Gly	Asp	Asn	Val	Lys	Ile	Leu	Asn	Ala	Asp	Asn	Val	Gln	Glu	Ala	Ala	435	440	445
Met	Glu	Thr	Asp	Gly	Tyr	Phe	Ile	Lys	Gly	Gly	Ile	Val	Thr	Val	Ile	450	455	460
Lys	Asp	Ala	Leu	Leu	Pro	Ser	Gly	Thr	Val	Ile						465	470	475

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<212> DNA
<213> zea mays

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ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat 240
attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaatth 300
aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac 360
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caggcacaca gagaacaaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa 600
cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct 660
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<211> 475

<212> PRT
<213> zea mays

<400> 4

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
1 5 10 15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
20 25 30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
245 250 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
275 280 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
290 295 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305 310 315 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
325 330 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
340 345 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
370 375 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385 390 395 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
405 410 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
420 425 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaagggtga 1380
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<212> PRT

<213> zea mays

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20 25 30

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly

	35					40					45				
Ile	Ile	Leu	Gly	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Lys
	50					55					60				
Lys	Arg	Ala	Lys	Pro	Ala	Val	Pro	Leu	Gly	Ala	Asn	Tyr	Arg	Leu	Ile
65					70					75					80
Asp	Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	Ile	Tyr
				85					90					95	
Val	Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Leu	Ser	Arg
			100					105					110		
Ala	Tyr	Gly	Ser	Asn	Ile	Gly	Gly	Tyr	Lys	Asn	Glu	Gly	Phe	Val	Glu
		115					120					125			
Val	Leu	Ala	Ala	Gln	Gln	Ser	Pro	Asp	Asn	Pro	Asn	Trp	Phe	Gln	Gly
	130					135					140				
Thr	Ala	Asp	Ala	Val	Arg	Gln	Tyr	Leu	Trp	Leu	Phe	Glu	Glu	His	Asn
145					150					155					160
Val	Met	Glu	Phe	Leu	Ile	Leu	Ala	Gly	Asp	His	Leu	Tyr	Arg	Met	Asp
				165					170					175	
Tyr	Glu	Lys	Phe	Ile	Gln	Ala	His	Arg	Glu	Thr	Asn	Ala	Asp	Ile	Thr
			180					185					190		
Val	Ala	Ala	Leu	Pro	Met	Asp	Glu	Lys	Arg	Ala	Thr	Ala	Phe	Gly	Leu
		195					200					205			
Met	Lys	Ile	Asp	Glu	Glu	Gly	Arg	Ile	Ile	Glu	Phe	Ala	Glu	Lys	Pro
	210					215					220				
Lys	Gly	Glu	Gln	Leu	Lys	Ala	Met	Met	Val	Asp	Thr	Thr	Ile	Leu	Gly
225					230					235					240
Leu	Asp	Asp	Val	Arg	Ala	Lys	Glu	Met	Pro	Tyr	Ile	Ala	Ser	Met	Gly
				245					250					255	
Ile	Tyr	Val	Phe	Ser	Lys	Asp	Val	Met	Leu	Gln	Leu	Leu	Arg	Glu	Gln
			260					265					270		
Phe	Pro	Glu	Ala	Asn	Asp	Phe	Gly	Ser	Glu	Val	Ile	Pro	Gly	Ala	Thr
		275					280					285			
Ser	Ile	Gly	Lys	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Glu
	290					295					300				
Asp	Ile	Gly	Thr	Ile	Ala	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	Thr
305					310					315					320
Lys	Lys	Pro	Ile	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Phe	Ala	Pro	Ile
				325					330					335	
Tyr	Thr	Gln	Pro	Arg	His	Leu	Pro	Pro	Ser	Lys	Val	Leu	Asp	Ala	Asn

340	345	350
Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys		
355	360	365
Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala		
370	375	380
Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu		
385	390	395 400
Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile		
405	410	415
Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg		
420		